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IN THE CLAIMS

Claims 1 – 11 withdrawn.

12. (AMENDED) An isolated polynucleotide encoding an enzymatically active variant of a [precursor] phenol oxidizing enzyme, [which precursor] wherein said phenol oxidizing enzyme has at least 68% identity to the amino acid sequence as disclosed in SEQ ID NO:2, said variant comprising a sequence that differs from that of said [precursor] phenol oxidizing enzyme in at least one of the positions 48, 67, 70, 76, 83, 98, 115, 119, 134, 171, 175, 177, 179, 188, 236, 246, 253, 254, 269, 272, 296, 302, 308, 318, 329, 331, 346, 348, 349, 365, 390, 391, 394, 404, 415, 423, 425, 428, 434, 465, 479, 481, 483, 499, 550, 562, 570, and 573, or sequence positions corresponding thereto.

13. (Original) An expression vector comprising the polynucleotide of claim 12.

14. (Original) A host cell comprising the expression vector of claim 13.

15. (Original) The host cell of claim 14, wherein said host cell is a filamentous fungus.

16. (Original) The host cell of claim 15, wherein said fungus is an *Aspergillus* species or a *Trichoderma* species.

17. Withdrawn

18. (AMENDED) A method for obtaining a phenol oxidizing enzyme variant [derived] from a *Stachybotrys* species, [said variant having at least one altered property relative to a precursor phenol oxidizing enzyme, which comprises] comprising the steps of:
mutagenizing a gene encoding [said precursor] a phenol oxidizing enzyme, which [precursor] phenol oxidizing enzyme comprises an amino acid sequence having at least 68% identity to the amino acid sequence shown in SEQ ID NO:2;

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introducing the mutant gene into a host strain whereby a transformed host strain is obtained;

growing said transformed host whereby said mutant gene is expressed and a phenol oxidizing enzyme variant, differing from said [precursor] phenol oxidizing enzyme by one or more amino acid substitutions, is identified by recovering said variant and screening it for increased phenol oxidizing activity and/or increased pH optimum.

19. (Original) The method of claim 18, wherein said one or more amino acid substitutions correspond to amino acid positions selected from the group consisting of 48, 67, 70, 76, 83, 98, 115, 119, 134, 171, 175, 177, 179, 188, 236, 246, 253, 254, 269, 272, 296, 302, 308, 318, 329, 331, 346, 348, 349, 365, 390, 391, 394, 404, 415, 423, 425, 428, 434, 465, 479, 481, 483, 499, 550, 562, 570, and 573 of said SEQ ID NO:2 sequence.

20. (Original) The method of claim 18, wherein said mutagenized gene is a cloned *Stachybotrys* gene, preferably a cloned *Stachybotrys chartarum* gene, or a cloned gene capable of hybridizing to such a *Stachybotrys* gene under conditions of intermediate to high stringency.

21. (AMENDED) A method for producing a variant of a [precursor] phenol oxidizing enzyme, which [precursor] enzyme comprises an amino acid sequence having at least 68% identity to the amino acid sequence shown in SEQ ID NO:2; said method comprising the steps of:

a) culturing a host cell comprising a polynucleotide encoding said variant, wherein said variant differs from said [precursor] phenol oxidizing enzyme sequence in at least one of the positions 48, 67, 70, 76, 83, 98, 115, 119, 134, 171, 175, 177, 179, 188, 236, 246, 253, 254, 269, 272, 296, 302, 308, 318, 329, 331, 346, 348, 349, 365, 390, 391, 394, 404, 415, 423, 425, 428, 434, 465, 479, 481, 483, 499, 550, 562, 570, and 573, or sequence positions corresponding thereto, under conditions suitable for the production of said variant; and

(b) optionally recovering said variant produced.

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Claims 22-24 withdrawn.

25. (NEW) The isolated polynucleotide of claim 12, wherein said polynucleotide encodes a variant which comprises a sequence that differs from that of the phenol oxidizing enzyme in at least one of the positions 254, 272, 346, 348, 394, and 425, or sequence positions corresponding thereto.

26. (NEW) The isolated polynucleotide of claim 12 wherein said polynucleotide encodes an amino acid substitution at one or more of the positions or position sets: 76/254/302; 76/254/302/188; 76/254/302/394/425; 119/254/329; 119/254/390; 119/254/415; 171/254/346; 236/254; 254; 254/272; 254/302/346/348; 254/346/348; 254/394; 254/550; and 394/425.

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27. (NEW) The isolated polynucleotide of claim 12 encoding a variant having at least one amino acid substitution or substitution set selected from:

N391S
G115S
D562G
D394N/V425M
V134I/H177Y
L499F
M254F
M254F/L499F
M98L/M254F
L76W/M254F
M254F/F349Y
H175V
H177V
L76W/M254F/E302V
M254F/D394N/V425M
L76W/M254F/E302V/D394N/V425M
M254F/A296S
M254F/W318Y
M254F/L48Y
M254F/R83K
M254F/M188F
M254F/Q246H
M254F/S331T
M254F/V483T
M254F/R67T
V119L/M254F/N70V
M254F/N70V
M254F/D308S
M254F/E365T
M254F/S415A
M254F/R423A
M254F/D428G
M254F/R434E
M254F/E465M
M254F/A479G
M254F/N550A
P253A
V119L/M254F/A269M
M254F/A269M
V119L/M254F/G329N
M254F/G329N
M254F/S331A

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M254F/E346V/E348Q
V119L/M254F/E346V
M254F/E346V
V119L/M254F/A390P
M254F/A390P
M254F/N404T
V119L/M254F/S415L
M254F/S415L
M254F/R481G
M254F/A573N
M254F/A573N/F570L
M254F/L76W/E302V/M188K
M254N
M254L
M254A
M254I
M254E
M254S
M254H
M254V
M254T
M254P
M254G
M254K
M254C
M254F/D394G
M254F/D394V
M254F/D394S
M254F/D394H
M254F/D394P
M254F/D394Y
M254F/D394W
M254F/D394N
M254F/M179F
M254F/M179V
M254F/M179P
M254F/M179G
M254F/M179E
M254F/M179L
M254F/I181D
M254F/S180F/I181L
M254F/E346V/E302I
M254F/E346V/E302K
M254F/E346V/E348Q/E302F

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M254F/E346V/E348Q/E302A
M254F/E346V/E348Q/E302L
M254F/E346V/E302C
M254F/E346V/E302V
M254F/E346V/M171T
M254F/E346V/E348Q/M171P
M254F/E346V/E348Q/M171L
M254F/E346V/M171Y
M254F/E346V/E348Q/M171V
M254F/E346V/M171S
M254F/E346V/M171R
M254F/E346V/E348Q/M171F
M254F/E346V/M171K
M254F/E346V/E348Q/M171Q
M254F/E346V/E348Q/M171N
M254F/E346V/E348Q/M171N/L172H
M254F/S272L
M254F/E236K
M254F/E346V/E348Q/M188K/D394W/S272L/E236K
M254F/E346V/E348Q/M188K/D394W/E236Q
M254F/E346V/E348Q/M188K/D394W/E236K
M254F/E346V/E348Q/M188K/D394W/E236D
M254F/E346V/E348Q/M188K/D394W/E236A
M188K/M254F/E346V/E348Q/D394W

28. (NEW) The isolated polynucleotide of any one of claims 12, 25, 26, or 27, wherein said phenol oxidizing enzyme has at least 80% identity, and preferably at least 85% identity, to the amino acid sequence disclosed in SEQ ID NO:2.

29. (NEW) The isolated polynucleotide of any one of claims 12, 25, 26, or 27, wherein the phenol oxidizing enzyme has at least 90% identity, and preferably at least 95% identity, to the amino acid sequence disclosed in SEQ ID NO:2.

30. (NEW) The isolated polynucleotide of claim 29, wherein the phenol oxidizing enzyme has the amino acid sequence disclosed in SEQ ID NO:2.

31. (NEW) The isolated polynucleotide of claim 12, wherein the phenol oxidizing enzyme variant has increased phenol oxidizing activity at high pH.

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32. (NEW) The isolated polynucleotide of claim 31, wherein the variant has a pH optimum of at least 8, and preferably at least 9.

33. (NEW) The isolated polynucleotide of claim 12, wherein said phenol oxidizing enzyme is obtainable from a *Stachybotrys* species, preferably *Stachybotrys chartarum*.

Respectfully submitted,

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